

Figure 1

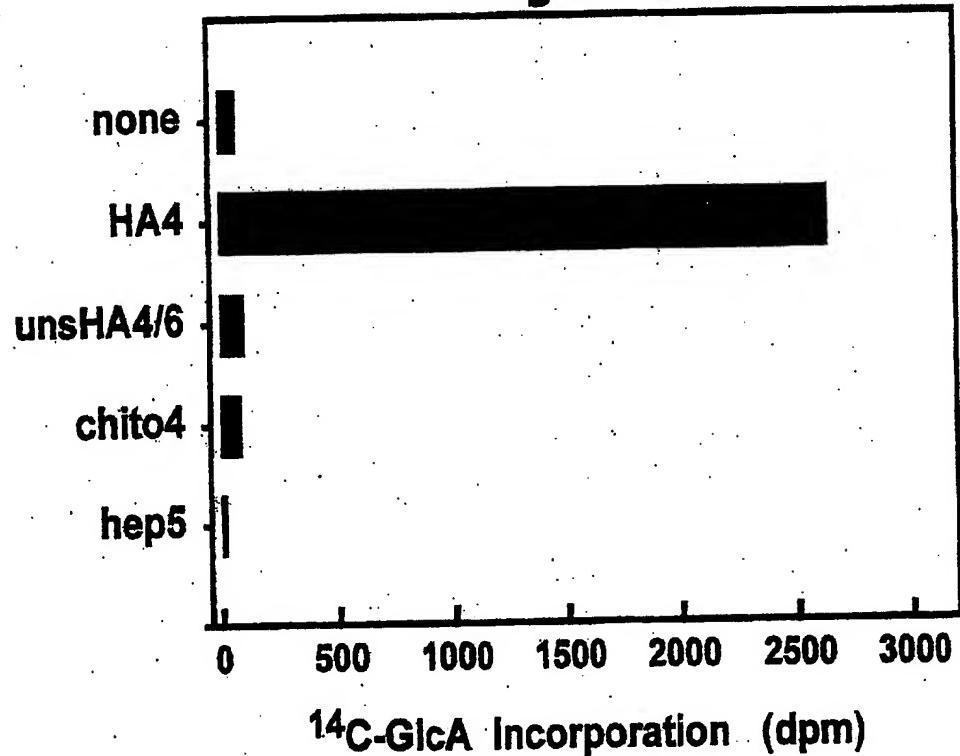
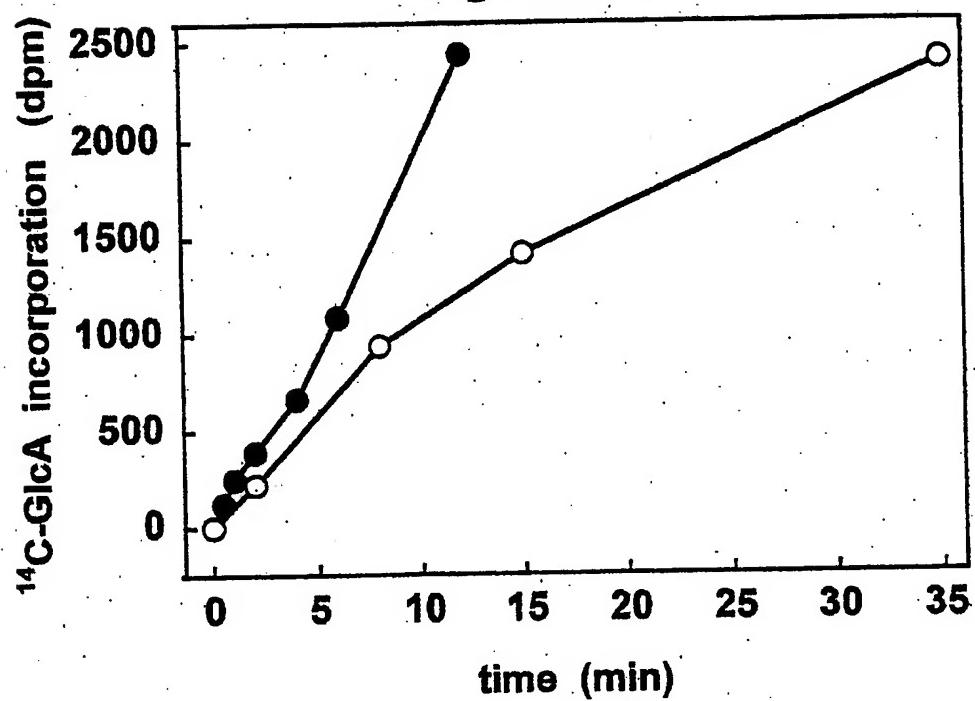


Figure 2



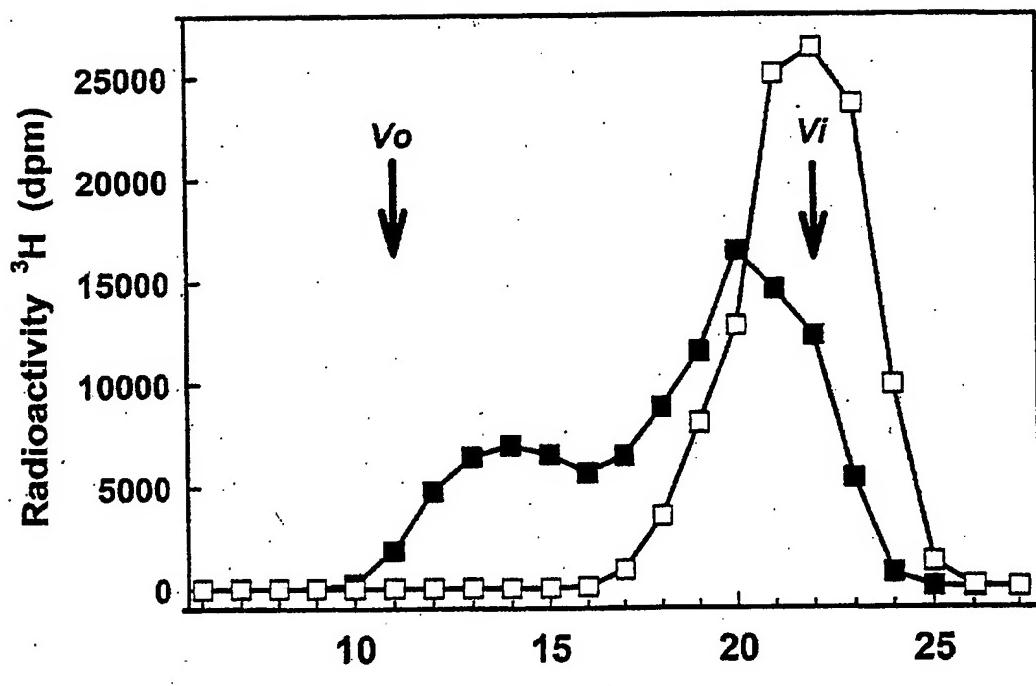
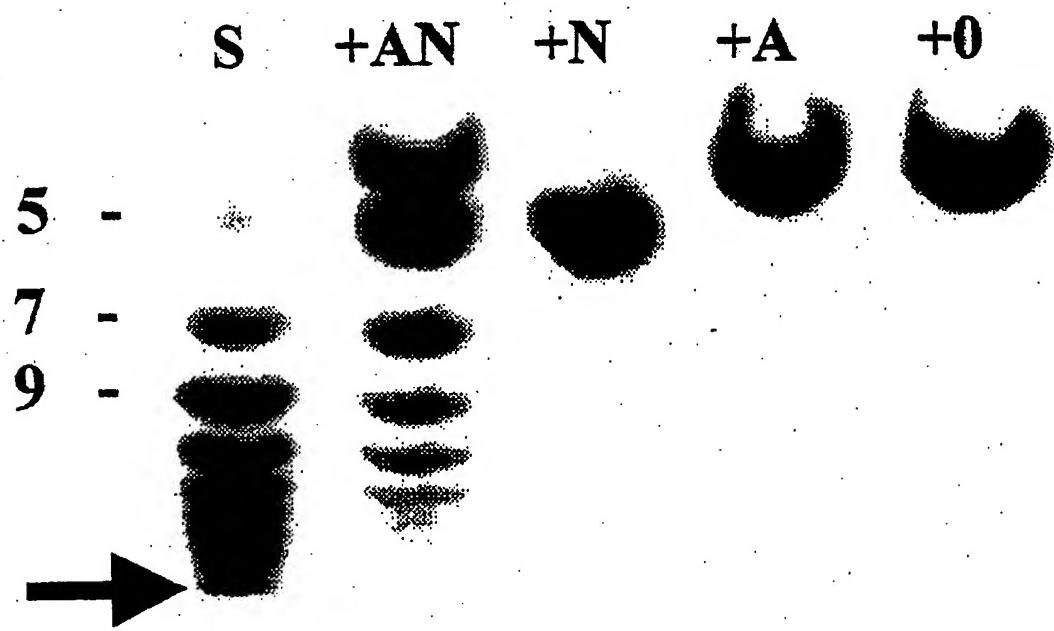


Figure 3

Figure 4

HA4 acceptor



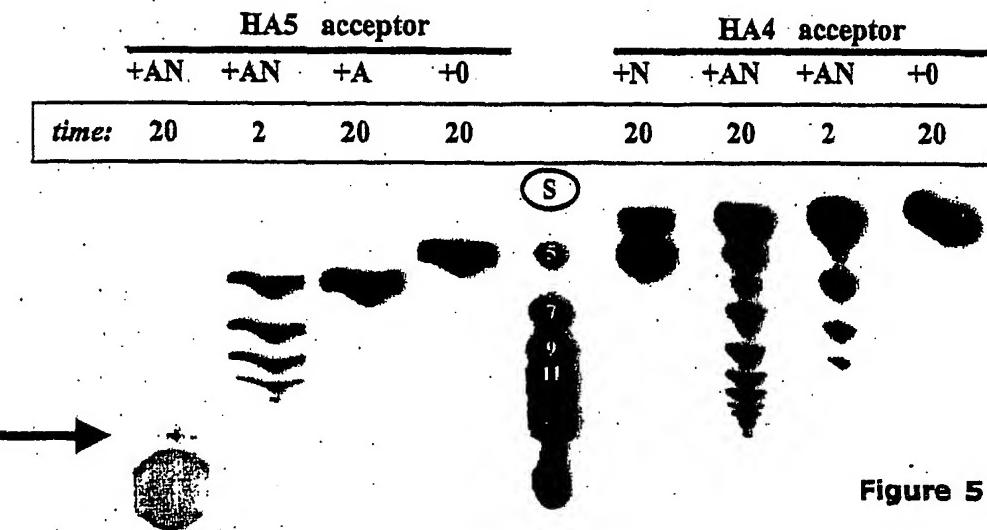


Figure 5

Ion Gel Filtration
Ex Fractions

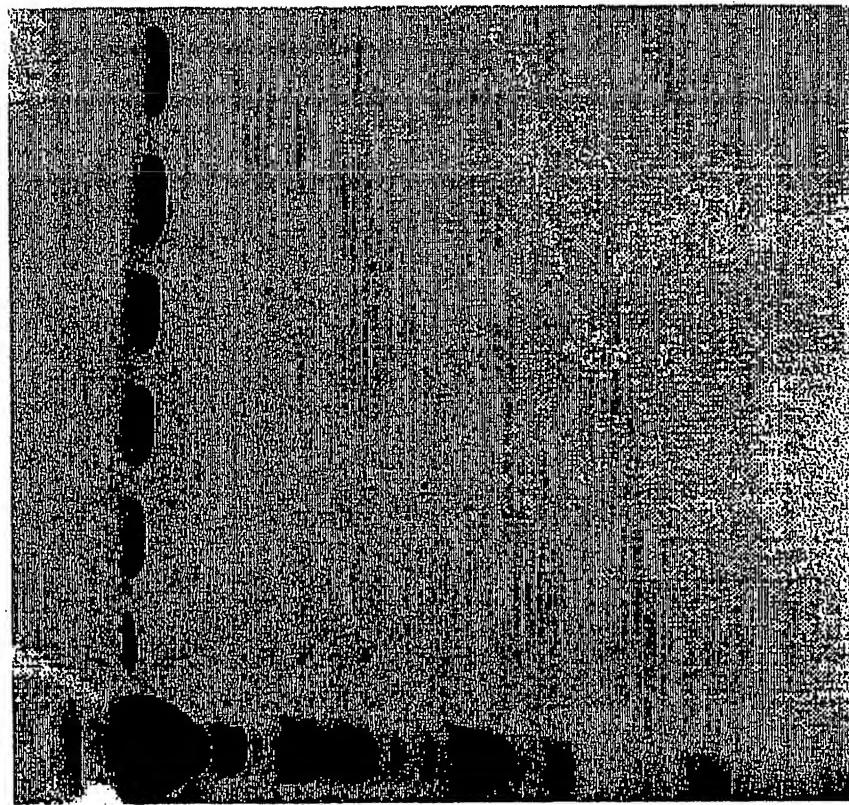
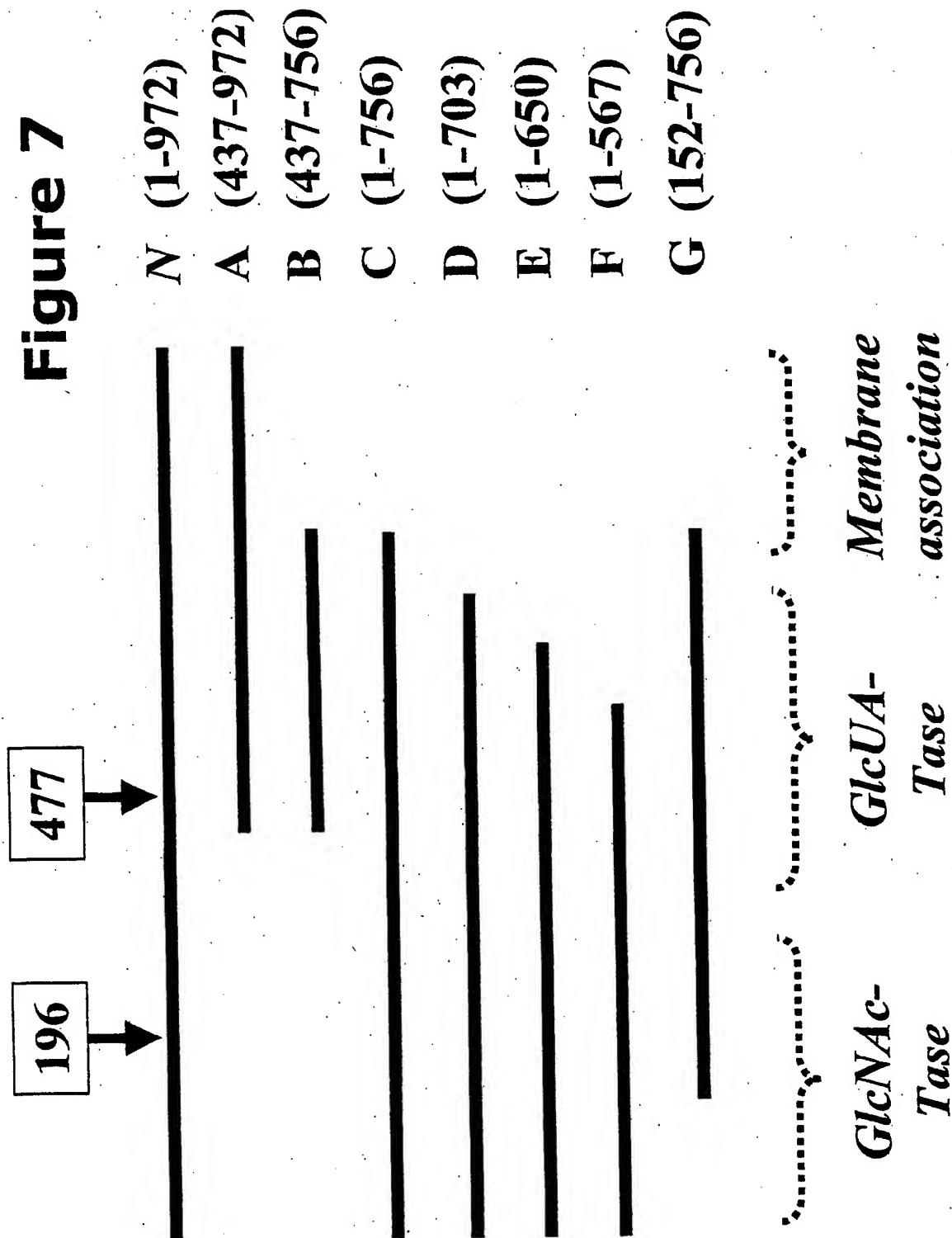


Figure 6

Figure 7



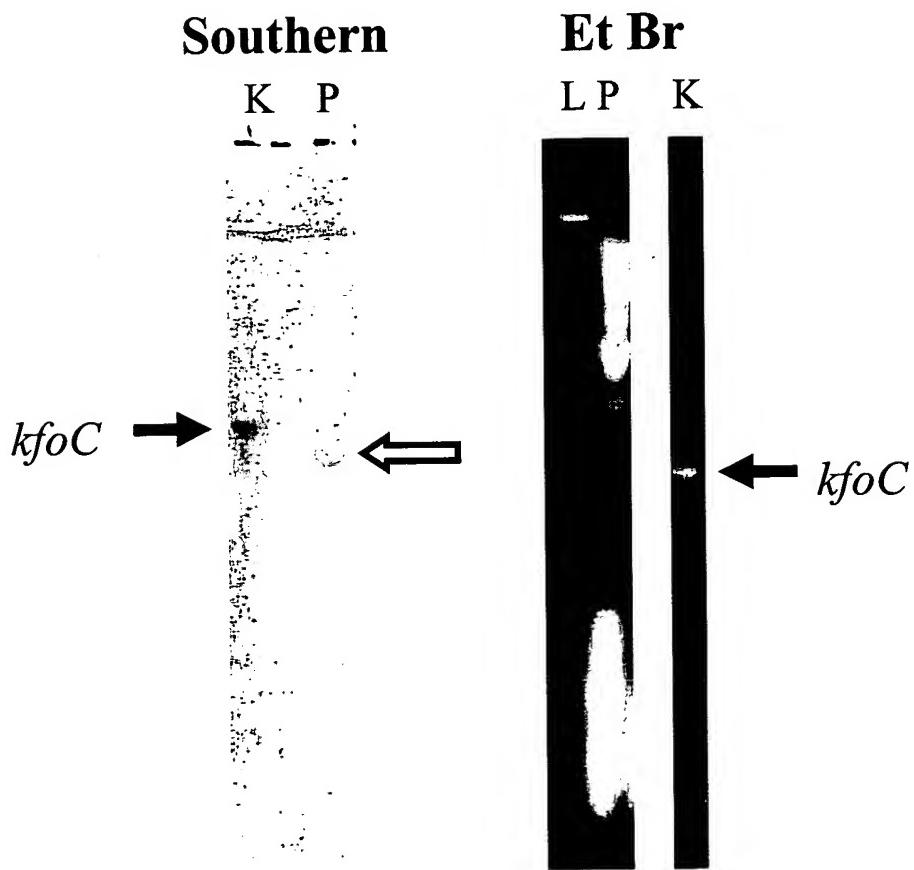


FIG. 8

Express Mail No.: EV272909140US Deposited: 08/15/2003
Title: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY
POLYMER GRAFTING AND METHODS OF MAKING AND USING
SAME
Inventors: Paul L. DeAngelis et al. Group: Unknown
Filed: Herewith Examiner: Unknown
Agent: Douglas J. Sorocco Dkt. No.: 3554.097
SHEET 9 OF 41 Formal Drawings

Figure 9

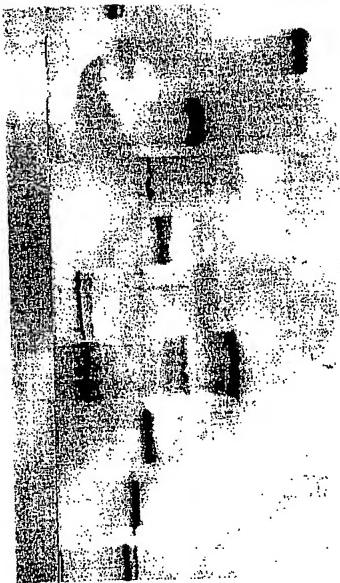


Figure 10

A

1 pmHAS 972

1 703 *PenHAsI-703*

Domain A2

D247249 D527/529

2

A1 SIVTTTENRPAILSTTLACLVNMQKTHYPFEVIVTD
A2 SIYIPAYNCANYIQRCVDSALNQ-TTVDLEVCICN

A1 DGSGEDLSPIRQYENKLDIYVRQKDNGFQASAAR
A2 DGSTDNTLEVINKLYGNNPVRVIMSKPNGGIASAS-

D247 / 249

A1 NMGLRLAKYDFIGLDDCDMAPNLWVHSYVAELLED
 A2 WAIVSEAEKGVYTGQI:DSDVY:EDDAVEI:CKKEEFLKD
 * * *

* * *
1527/529

Figure 11

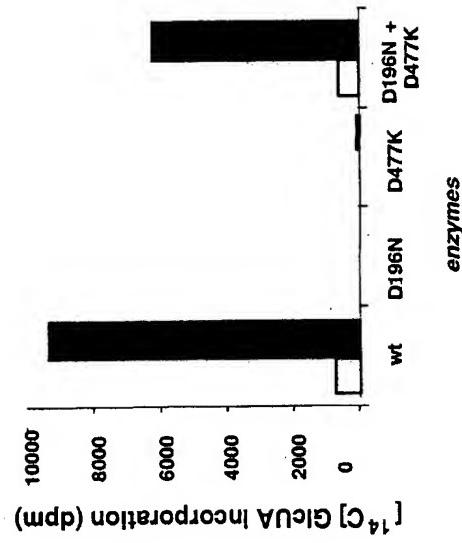


Figure 12

| | |
|---------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| pmCS pmHAS | 1. MNTLSQATKA YNSNDYELAL KLFTEKSAETY GRKIVEFGII ECKEKLSTNS 50 Q----I-----T-----AHP |
| pmCS pmHAS | 51. IVS----- HDEKKNVSQDS SLDITATOLLE SNVRKLTSE SERNSIXNKR 100 S-NSAHTSVN KEEVN P-----V-B-----T----- |
| pmCS pmHAS | 101. KSITGRKSEN AEIRKVELVP KDFPKDENVLA PLFDHVNDFT WYKGNRKKSLG 150 -LL-E-----V-A-A-----L-----K-----R----- |
| pmCS pmHAS | 151. IKPVVNKGIGL SILLPTENRS RILDITIACL VNQKTNYPFE VVVADDGSKE 200 ---EHQH----VT-----P A-S-----H-----I-T-----Q----- |
| pmCS pmHAS | 201. NELETIVORVE QKLDIKEYVRO KDKGYOLCAV RNGLGLRTAKY DFVSIILDCDM 250 D-SP-IRQ--N----R---N-F-RS-A--M---L---IGL----- |
| pmCS pmHAS | 251. APQQLWVHSY LTTEILEDNDI VLIIGPRKRYD THNITTAEQJL NDFPYLIESLP 300 --NP-----VA-----D-L T-----I-----QH-DEKD---MAS-L----- |
| pmCS pmHAS | 301. ETATNNNEPI TSKGNISLDW RLEHFAKTDN IRLCDSPFRY FVAGNVAFSK 350 -VK---SVAA KGE-TV---Q-I-E---S-----T-----A-----A----- |
| pmCS pmHAS | 351. EWLINKVQHFD KEFNRHWGGED VEGYTRLEAK GCERFRVIDGG MAYHQEPGK 400 K---S-F---R-----S-----KT-----I-----Y----- |
| pmCS pmHAS | 401. ENETTEREACK SITLKIVREK VPVITYRMLLP LEDSHIRHRP LVSVIYPAVN 450 ---D-----N---D-MR---N-----N-V----- |
| pmCS pmHAS | 451. CANYIQRVCVD SALNQTVVDL EVCICNDGST DNTLEVINKL YGNNNPRVRIM 500 ----- |
| pmCS pmHAS | 501. SKPNNGGIASA SNAAVSFAKG YYIGQLSDDD YLEPDAVELC EREFIUKDKTL 550 ----- |
| pmCS pmHAS | 551. ACVYTTTNRNV NPDGSLIANG YNWPEESREK LTTAMIAHHT RMFTTIRANHL 600 ----- |
| pmCS pmHAS | 601. TDGFNMENIEN AVDYOMFLKL SEVGKEKHLN KICYNRVLHG DNTSIKKLG 650 -----K----- |
| pmCS pmHAS | 651. QXKNHITVVVN QSLMRQGINT YNYDKEDDID ESRKYIFNKT AEYQREMMDML 700 -----T-----E-----I-----I----- |
| pmCS pmHAS | 701. KDLKLQIQKD AKIAVSIIFP NTINGLVKKL NMIEYENKNI FVIIILHVDKN 750 ---I-I-----V----- |
| pmCS pmHAS | 751. HLTRDIKEI LAFYHKHQVN ILLNNDISYY TSNRLIKTEA HLSNINKLSD 800 ----- |
| pmCS pmHAS | 801. LININCEYITF DNHDLSLFVN DSXAYMKYD VGMNESALTH DWIEKINAHP 850 ----- |
| pmCS pmHAS | 851. PFKKLKLIKTYF NDNDLRSMV KGASQGMIMK YALPHELLTI IKEVITSQS 900 -----K-----T-----A----- |
| pmCS pmHAS | 901. IDSVPEYNTF DIWFQFALLI LEKKTIGHVFN KTSTLTYPFW ERKLOWTNEQ 950 ----- |
| pmCS pmHAS | 951. IQSARRGENI PVNKFIINSI TL 972 -----E-----R----- |

Figure 13

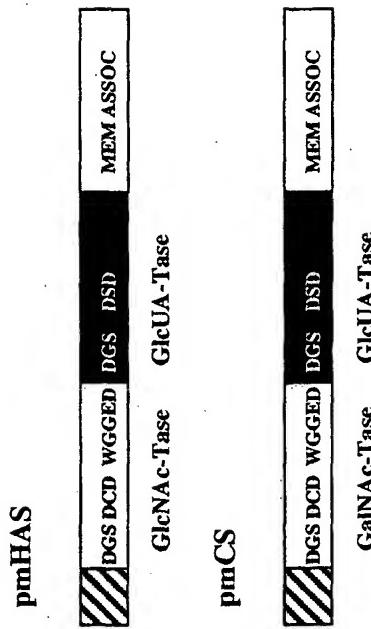


Figure 14

Express Mail No.: EV272909140US Deposited: 08/15/2003
 Title: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY
 POLYMER GRAFTING AND METHODS OF MAKING AND USING
 SAME

Inventors: Paul L. DeAngelis et al. Group: Unknown
 Filed: Herewith Examiner: Unknown
 Agent: Douglas J. Sorocco Dkt. No.: 3554.097
 SHEET 14 OF 41 Formal Drawings

| | | | | |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 91 HS1 Kf1C con 140 APPLVSIIMTSHTNEKFIEASINSLLQTYNNLEVIVVDDYSTSTDKTFQIA GKDLVSIIMSVFNSEDTIAYSLHSLLNQTYENIEILVCDCCSSDKSLEII ..LVSII..N*E..I..S..SLL.QTY#N.E!..V..DD..S*DK*.#I. | 190 HS1 Kf1C con 141 SRIANSTSKVKTFRILNSNLGTYFAKNTGILKSKGDIIFFQDSDDVCHHER KSIAYSSSSRVRKVYSSSRKNQGPYNIRNELLKAHGNFITFQDADDLSHPER ..IA.S*S*VK.%...N.G;Y...N..I.K..G#.I.FQD.DD..H.ER | 240 HS1 Kf1C con 191 IERCVNALLSNKDNIAVRCAYSRINLETQNIKVNDNKYKLGGLITLGVYR IQRQVEVLRNNKAVICM.ANWRVASNGKIOFFYDDKATRMSVSSMIKK I#R.V#.L..NK..I.....R!.#.....#D....*\$...!*...!..*. | 490 HS2 Kf1A con 441 YITCDDDIRYPADYINTMIKKINKYND.KAAIGLHGVIFPSRVNKYFSSD IVLTDDDIYPPDYVEKMLNFYNSFAIFNCIVGIHGCIYIDAFDGD.QSK .!..DDDI.YP.DY!#.M....N.%....!G.HG.I%....#....S. | 540 HS2 Kf1A con 491 RIVYNFQKTFRKDTAVNILGTGTVAFRVSIFNKFSLSDFEHPGMVDIYFS RKVFSFTQGLLRPRVWNQLGTGTVFLRAQDQLPSLRYMDGSQR.FVDVRF R.V%..F.....*....VN.LGTGTV...*.....D.....VD!.FS |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

Figure 14 cont'd

617

1

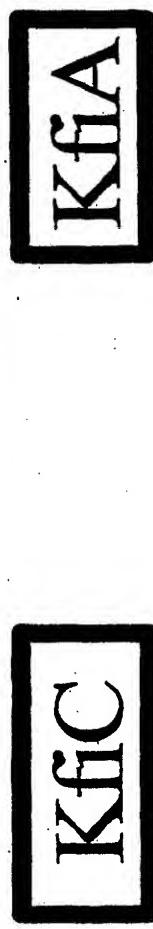


Figure 15A

Figure 15B

| | |
|---------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| pmHS pg1A DcbF Consensus | 1 10 20 30 40 50 60 70 <hr/> MSLFKRATELFKSGNYKDALTLYENIARIKYG—SESLVKYNIDI MKRKKEMTQKQMTKNPPQHEKENELNTFQNKIDSLSKTTLNKDIISQQTLAKQDSKHPLSASLENEKLL MSLFKRATELFKSGNYKDALTLYENIARIKYG—SESLVKYNIDI \$slFkrat#lfKsgnyKDaltlyeniARIkyg...SeSlVkyNidi |
| pmHS pg1A DcbF Consensus | 71 80 90 100 110 120 130 140 <hr/> CKK-NITQSNSKIEEDNISGENKF—SVSIKOLYNEISSELGITKERLGAPPVLVSIIIMTSHNTEK LKQLQLVLQEFEKIYTQNQALEKLDKQTTSITOLYNEVAKSDLGLVKETNSVNPLVSIIIMTSHNTEQ CKK-NITQSNSKIEEDNISGENEF—SVSIKOLYNEISSELGITKERLGAPPVLVSIIIMTSHNTEK cKk.#itqsk#KIEedNisgEnkf....svSIkOLYNEIsnS#LGIkerleapPLYSIIIMTSHNTEk |
| pmHS pg1A DcbF Consensus | 141 150 160 170 180 190 200 210 <hr/> FIERASINSLLLQTYNNLEVIVVDDYSTDOKTFQIASRIANSTSALKTFRRLNSNLGTYFAKNTGILSKKGDI FIERASINSLLLQTYNNLEVIVVDDYSTDOKTFQIASRIANSTSALKTFRRLNSNLGTYFAKNTGILSKKGDI FIERASINSLLLQTYNNLEVIVVDDYSTDOKTFQIASRIANSTSALKTFRRLNSNLGTYFAKNTGILSKKGDI FIERASINSLLLQTYNNLEVIVVDDYSTDOKTFQIASRIANSTSALKTFRRLNSNLGTYFAKNTGILSKKGDI |
| pmHS pg1A DcbF Consensus | 211 220 230 240 250 260 270 280 <hr/> IFFQDSDDVCHHERIERCVCNALLSNKDNIAVRAYSRINLETQKQDCKVNDNQYKLGILITLGvYRKVFNEI IFFQDSDDVCHHERIERCVCNILLANKETIAVRAYSRILAPETQKQDCKVNNMDYRLGFITLGHHRKVFQEI IFFQDSDDVCHHERIERCVCNALLSNKDNIAVRAYSRINLETQKQDCKVNDNQYKLGILITLGvYRKVFNEI IFFQDSDDVCHHERIERCVCNALLSNKDNIAVRAYSRINLETQKQDCKVNDNQYKLGILITLGvYRKVF#EI |
| pmHS pg1A DcbF Consensus | 281 290 300 310 320 330 340 350 <hr/> GFFNCTTKASODDEFYHRIIKYYGKRNINNLFLPLYYNTMREDSLFSOMVENVDENNIKQKTSORRQNYLH GFFNCTTKGSODEFFHRIIKYYGKEKIKHLLLPLYYNTMRENSLTDMVYEHDDNNIKQMSDTROHYAT GFFNCTTKASODDEFYHRIIKYYGKRNINNLFLPLYYNTMREDSLFSOMVENVDENNIKQKTSORRQNYLH GFFNCTTKAsODDEFXHRIIKYYGK#-InNLfLPLYYNTMRE#SLF#DMVENVDENNIKQKTSORRQnY1h |
| pmHS pg1A DcbF Consensus | 351 360 370 380 390 400 410 420 <hr/> EFQKJHNERKLNELKEIIPSFPRIDALPISKEMSKLSPNPKIPVYINICSIIPSRIKOLQYTIIGVLKNQCDH LFQRMHNETRASHDFKLQFQPRIDALPVPQEMSKLSPNPKIPVYINICSIIPSRIKOLRRIIGILKNQCDH EFQKJHNERKFNELKEIIPSFPRIDALPISKEMSKLSPNPKIPVYINICSIIPSRIKOLQYTIIGVLKNQCDH eFQkJHNERk#1K#I&F&PRIDALPiskemsklspnpkipvyinicsipsrikolqytiigvlknqcdh |
| pmHS pg1A DcbF Consensus | 421 430 440 450 460 470 480 490 <hr/> FHIVLDGYPEVPDFIFIKKLGKMKATVINCQNKNESIRDNGKFILEKLKENKDGYYITCDDDIRYPADYTN FHIVLDGYPEVPDFIFIKKLGKMKATVINCQNKNESIRDNGKFILEKLKENKDGYYITCDDDIRYPADYIN FHIVLDGYPEVPDFIFIKKLGKMKATVINCQNKNESIRDNGKFILEKLKENKDGYYITCDDDIRYPADYIN FHIVLDGYPEVPDFIFIKKLGKMKATV!nCq#K#SIRDNGKFILEKLKENKDGYYITCDDDIRYPADYIN |
| pmHS pg1A DcbF Consensus | 491 500 510 520 530 540 550 560 <hr/> THIOKKKINKYMDKRAIGLHGVIIFPSRVNKYFSSDRIVYHNFQKPLENDTAVNLLGTGTvFRYSIFNKFSLS THIOKKLNEYDKRAIGLHGIIIFPSRVNKYFSSDRIVYHNFQKTRK THIOKKKINKYMDKRAIGLHGVIIFPSRVNKYFSSDRIVYHNFQKTRK THIOKKLNEYDKRAIGLHGVIIFPSRVNKYFSSDRIVYHNFQKTRK |
| pmHS pg1A DcbF Consensus | 561 570 580 590 600 610 620 630 <hr/> DFEHPGMVDIYFSILCKKKNIlQCVISRPWHLTEDNKTETLFHEFQNRDEIQSKLITSSNNPHGYSSIY DFTHSGMADIYFSILCKKKNIlQCIISRPWHLTEDNROSETLYHQYRDNDEQQTQLIMENGPHGYSSIY |
| pmHS pg1A DcbF Consensus | 631 640 651 <hr/> df.h.gn.diyfs.lckkknlq.cisrp.nultedn...etl.h....de.q..li...n.pugyzziy PLLNNNANYSSELIPCLSFYNE PLVKNHPKFTDILIPCLPFYFL Consensus pl...n.....lipcl.fy.. |

Figure 15C

Multalin version 5.4.1

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Published research using this software should cite.

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

is anyone of NDQEBZ

MSF: 651 Check: 0

| | | | |
|-----------------|----------|-------------|--------------|
| Name: A | Len: 651 | Check: 612 | Weight: 0.58 |
| Name: B | Len: 651 | Check: 249 | Weight: 0.58 |
| Name: pg1A | Len: 651 | Check: 7677 | Weight: 1.08 |
| Name: DcbF | Len: 651 | Check: 7537 | Weight: 1.76 |
| Name: Consensus | Len: 651 | Check: 5816 | Weight: 0.00 |

//

| | | |
|-----------|----------------------------------------------------------|-------------------------------|
| | 1 | 50 |
| A2 | | MSLFKR ATELFKSGNY KDALTLYENI |
| B10 | | MSLFKR ATELFKSGNY KDALTLYENI |
| pg1A | MKRKKEMTQK QMTKNPPQHE KENEINTFQN KIDSLLKTTLN KDIISQQTILL | |
| DcbF | | MSLFKR ATELFKSGNY KDALTLYENI |
| Consensus | | \$s1fkr at#lfKsgny KDaltlyeni |
| | 51 | 100 |
| A2 | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.... | |
| B10 | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.... | |
| pg1A | AKQDSKHPLS ASLENENKLL LKQLQLVLQE FEKIYTYNQA LEAKLEKDKQ | |
| DcbF | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENEF.... | |
| Consensus | AKIyg....S eSLvkyNidi cKk.#itqsk s#KieedNis gEnkf.... | |
| | 101 | 150 |
| A2 | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL | |
| B10 | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL | |
| pg1A | TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSHNTAQ FIEASINSLL | |
| DcbF | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL | |
| Consensus | svSIkDLYNE !snS#LGitK ErlgapPLVs IIMTSHNTek FIEASINSLL | |
| | 151 | 200 |
| A2 | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTyFAKN | |
| B10 | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTyFAKN | |
| pg1A | LQTYKNIEII IVDDDSSDNT FEIASRIANT TSKVRVFRNL SNLGTyFAKN | |
| DcbF | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTyFAKN | |
| Consensus | LQTYnN1E!I !VDDyStDkt F#IASRIANs TSKVktFRNL SNLGTyFAKN | |

Fig. 15C cont'd

| | |
|------------------------------------------------------------------|-----|
| 201 | 250 |
| A2 TGILKSKGDI IFFQDSDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL | |
| B10 TGILKSKGDI IFFQDSDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL | |
| pg1A TGILKSKGDI IFFQDSDVC HHERIERCVN ILLANKETIA VRCAYSRLAP | |
| DcbF TGILKSKGDI IFFQDSDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL | |
| Consensus TGILKSKGDI IFFQDSDVC HHERIERCVN aLLsnk#nIA VRCAYSRin1 | |
| | |
| 251 | 300 |
| A2 ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK | |
| B10 ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK | |
| pg1A ETOHIIKVNN MDYRLGFITL GMHRKVFQEI GFFNCTTKGS DDEFFHRIAK | |
| DcbF ETOHIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK | |
| Consensus ETQnIiKVN# nkYkLGltl GvYRKVF#EI GFFNCTTKaS DDEF%HRIIK | |
| | |
| 301 | 350 |
| A2 YYGKNRINNL FPLYYNTMR EDSLFSDMVE WVDENNIKQK TSDARQNYLH | |
| B10 YYGKNRINNL FPLYYNTMR EDSLFSDMVE WVDENNIKQK TSDARQNYLH | |
| pg1A YYGKEKIKNL LLPYYNTMR ENSLFTDMVE WIDNHNIIQK MSDTRQHYAT | |
| DcbF YYGKNRINNL FPLYYNTMR EDSLFSDMVE WVDENNIKQK TSDARQNYLH | |
| Consensus YYGK#rInNL FPLYYNTMR E#SLFSDMVE W!D#nNIKQK tSDaRQnYlh | |
| | |
| 351 | 400 |
| A2 EFQKIHNERK LNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI | |
| B10 EFQKIHNERK LNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI | |
| pg1A LFQAMHNETA SHDFKNLFQF PRIYDALPVP QEMSKLSNPK IPVYINICSI | |
| DcbF EFQKIHNERK FNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI | |
| Consensus eFQkiHNERk .n#1K#iFsf PRIHDALP!s KEMSKLSNPK IPVYINICSI | |
| | |
| 401 | 450 |
| A2 PSRIKQLQYT IGVLKNCQDH FHIYLDGYPE VPDFIKKLGN KATVINCQNK | |
| B10 PSRIKQLQYT IGVLKNCQDH FHIYLDGYPE VPDFIKKLGN KATVINCQNK | |
| pg1A PSRIAQLRRRI IGIKNOCQDH FHIYLDGYVE IPDFIKNLGN KATVVKCKDK | |
| DcbF PSRIKQLQYT IGVLKNCQDH FHIYLDGYPE VPDFIKKLGN KATVINCQNK | |
| Consensus PSRIKQLqyt IG!LKNQCDH FHIYLDGYpE !PDFIKKLGN KATV!nCq#K | |
| | |
| 451 | 500 |
| A2 NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYTN TMIKKINKYN | |
| B10 NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN | |
| pg1A DNSIRDNGKF ILLEKLIKEN QDGYYITCDD DIIYPSDYIN TMIKKLNeyD | |
| DcbF NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN | |
| Consensus ##SIRDNGKF ILLEkLIken KDGYYITCDD DIRYPADYIN TMIKKLNky# | |
| | |
| 501 | 550 |
| A2 DKAAGLHGKV IFPSRVNKYF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR | |
| B10 DKAAGLHGKV IFPSRVNKYF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR | |
| pg1A DKAVIGLHGI LFPSRMTKYF SADRIVYSFY KPLEKDKAVN VLGTGTVSFR | |
| DcbF DKAAIGLHGKV IFPSRVNKYF SSDRIVYNFQ KTFRK..... | |
| Consensus DKAAGLHG! IFPSRVnKYF SsDRivYnFq Kplekd.avn .lgtgtv.fr | |
| | |
| 551 | 600 |
| A2 VSIFNFKSLS DFEHPGMVDI YFSILCKKNN ILQVCISRPS NWLTEDNKN | |
| B10 VSIFNFKSLS DFEHPGMVDI YFSILCKKNN ILQVCISRPS NWLTEDNKN | |
| pg1A VSLFNQFSLS DFTHSGMADI YFSLLCKKNN ILQICISRPA NWLTEDNRDS | |
| DcbF | |
| Consensus vs.fn.fsls df.h.gm.di yfs.lckknn ilq.cisrp. nwltedn... | |

Fig. 15C c nt'd

| | |
|----------------------------------------------------------------|-------|
| 601 | 650 |
| A2 ETLFHEFQNR DEIQSKLIIS NNPWGYSSIY PLLNNNANYS ELIPCLSFYN | |
| B10 ETLFHEFQNR DEIQSKLIIS NNPWGYSSIY PLLNNNANYS ELIPCLSFYN | |
| pg1A ETLYHQYRDN DEQQTQLIME NGPVGYSSIIY PLVKNHPKFT DLIPCLPFYF | |
| DcbF | |
| Consensus etl.h.... de.q..li... n.pwgyssiy pl..n.... lipcl.fy. | |
| 651 | |
| A2 E | |
| B10 E | |
| pg1A L | |
| DcbF . | |
| Consensus . | |

Figure 15D

Multalin version 5.4.1

Copyright I.N.R.A. France 1989, 1991, 1994, 1996

Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

is anyone of NDQEBZ

MSF: 651 Check: 0

| | | | |
|-----------------|----------|-------------|--------------|
| Name: pmHS | Len: 651 | Check: 612 | Weight: 0.75 |
| Name: pg1A | Len: 651 | Check: 7677 | Weight: 0.75 |
| Name: DcbF | Len: 651 | Check: 7537 | Weight: 1.49 |
| Name: Consensus | Len: 651 | Check: 5816 | Weight: 0.00 |

//

| | | |
|-----------|---------------------------------------------------------|-------------------------------|
| | 1 | 50 |
| pmHS | | MSLFKR ATELFKSGNY KDALTLYENI |
| pg1A | MKRKEMTQK QMTKNPPQHE KENELENFTQNL KIDSLLTTLN KDIISQQTLL | |
| DcbF | | MSLFKR ATELFKSGNY KDALTLYENI |
| Consensus | | \$s1fkr at#lfKsgny KDaltlyeni |
| | 51 | 100 |
| pmHS | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.... | |
| pg1A | AKQDSKHPPLS ASLENENKLL LKQLQLVLOE FEKIYTQNA LEAKLEKDKQ | |
| DcbF | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENEF.... | |
| Consensus | AKiyg....S eSLvkyNidi cKk.#itqsk s#KieedNis gEnkf.... | |
| | 101 | 150 |
| pmHS | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSNTEK FIEASINSLL | |
| pg1A | TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSNNTAQ FIEASINSLL | |
| DcbF | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSNTEK FIEASINSLL | |
| Consensus | svSIKDLYNE !snS#LGitK ErlgapPLVS IIMTSNNTek FIEASINSLL | |
| | 151 | 200 |
| pmHS | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN | |
| pg1A | LQTYKNIEII IVDDDSSDNF FEIASRIANT TSKVRVFRNL SNLGTYFAKN | |
| DcbF | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN | |
| Consensus | LQTyNnE!I !VDDyStDkt F#IASRIANs TSKVktFRNL SNLGTYFAKN | |
| | 201 | 250 |
| pmHS | TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL | |
| pg1A | TGILKSKGDI IFFQDSDDVC HHERIERCVN ILLANKETIA VRCAYSRIAP | |
| DcbF | TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL | |
| Consensus | TGILKSKGDI IFFQDSDDVC HHERIERCVN aLLsNK#nIA VRCAYSrInl | |
| | 251 | 300 |
| pmHS | ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK | |
| pg1A | ETOIIIKVNN MDYRLGFITL GMHRKVQEI GFFNCTTKGS DDEFYHRIAK | |
| DcbF | ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK | |
| Consensus | ETQnIIKVn# nkYKLGLITL GvyRKVF#EI GFFNCTTKAs DDEFYHRIIK | |

Figure 15D

| | |
|------------------------------------------------------------------|-----|
| 301 | 350 |
| pmHS YYGKNRINNL FLPLYYNTMR EDSLFSMDMVE WVDENNIKQK TSDARQNYLH | |
| pg1A YYGKEKIKNL LLPLYYNTMR ENSLFTDMVE WIDNHNIIQK MSDTRQHYAT | |
| DcbF YYGKNRINNL FLPLYYNTMR EDSLFSMDMVE WVDENNIKQK TSDARQNYLH | |
| Consensus YYGK#rInNL flPLYYNTMR E#SLFsDMVE W!D#nNIkQK tSDaRQnYh | |
| | |
| 351 | 400 |
| pmHS EFQKIHNERK LNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI | |
| pg1A LFQAMHNETA SHDFKNLFQF PRIYDALPVP QEMSKLSNPK IPVYINICSI | |
| DcbF EFQKIHNERK FNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI | |
| Consensus eFQkiHNERk .n#lK#iFsF PRIhDALP!s KEMSKLSNPK IPVYINICSI | |
| | |
| 401 | 450 |
| pmHS PSRIKQLQYT IGVLKNQCDH FHIYLDGYPE VPDFIKKLGN KATVINCQNK | |
| pg1A PSRIAQLRRRI IGILKNQCDH FHIYLDGYVE IPDFIKNLGN KATVVHCKDK | |
| DcbF PSRIKQLQYT IGVLKNQCDH FHIYLDGYPE VPDFIKKLGN KATVINCQNK | |
| Consensus PSRIkQLqyt IG!LKNQCDH FHIYLDGypE !PDFIKkLGN KATV!nCq#K | |
| | |
| 451 | 500 |
| pmHS NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYTN TMIKKINKYN | |
| pg1A DNSIRDNGKF ILLEELIEKN QDGYYITCDD DIIYPSDYIN TMIKKLNNEYD | |
| DcbF NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN | |
| Consensus ##SIRDNGKF ILLEkLIken xDGYYITCDD DIRYPaDYiN TMIKKINKY# | |
| | |
| 501 | 550 |
| pmHS DKAAIGLHGv IFPSRVNKyF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR | |
| pg1A DKAVIGLHG1 LFPSRMTKYF SADRIVYSFY KPLEKDKAVN VLGTGTVSFR | |
| DcbF DKAAIGLHGv IFPSRVNKyF SSDRIVYNFQ KTFRK..... | |
| Consensus DKAaIGLHG! iFPSRvnKYF SsDRiVYnFq Kplekd.avn .lgtgtv.fr | |
| | |
| 551 | 600 |
| pmHS VSIFNKFSLs DFEHPGMVDI YFSILCKKNN ILQVCISRPS NWLTEDNKNT | |
| pg1A VSLFNQFSLS DFTHSGMADI YFSLLCKKNN ILQICISRPA NWLTEDNRDS | |
| DcbF | |
| Consensus vs.fn.fs1s df.h.gm:di yfs.lckknn ilq.cisrp. nwltedn... | |
| | |
| 601 | 650 |
| pmHS ETLFHEFQNR DEIQSKLIIS NNPWGYSSIY PLLNNNANYS ELIPCLSFYN | |
| pg1A ETLYHQYRDN DEQQTQLIME NGPWGYSSIY PLVKNHPKFT DLIPCLPFYF | |
| DcbF | |
| Consensus etl.h..... de.q..li.. n.pwgysiiy pl...n.... lipcl.fy. | |
| | |
| 651 | |
| pmHS E | |
| pg1A L | |
| DcbF . | |
| Consensus . | |

Figure 16

| enzyme | activity |
|-------------------------------------------------------------------------------------|------------|
| pmHAS 1-703 | HAS |
| pmCS 1-704 | CS |
|  | |
| pm-EG | GlcUA-Tase |
| pm-FH | CS |
|  | |
| pm-IK | GlcUA-Tase |
| pm-JL | HAS |

Figure 17

| | 211 | 220 | 230 | 240 | 250 |
|--------------------|-------------------------------------------|-----|-----|-----|-----|
| P _n HAS | NKLDIYRYRQKDNGFQASAARRNMGRLAKYDFIGLLDCDHI | | | | |
| P _n CS | QKLDIKEYRQKDGYQLCAVRNLGLRTAKYDFYSILDCDMI | | | | |
| Turkey | EKLDIKEYRQKDGYQLCAVRNLGLRTAKYDFYSILDCDM | | | | |
| Goose | VDIKYYRQKDGYQLCAVRNLGLRTAKYDFYSILDC | | | | |
| Sea-lion | KYYRQKDGYQLCAVRNLGLRTAKYDFYSILDC | | | | |
| Consensus | ...dikYYRQKDyG%Q1cAvRN\$GLRtAKYDF!siLDC.. | | | | |
| mutant 1 | ★ | | | | |
| mutant 2 | | ★ | | | |
| mutant 3 | | ★ | | | |
| mutant 4 | ★ | ★ | | | |
| mutant 5 | ★ | ★ | | | |
| mutant 6 | | ★★ | | | |
| mutant 7 | ★ | ★★ | | | |
| mutant 8 | | | | | ★ |
| mutant 9 | | | | | ★★ |

Figure 18

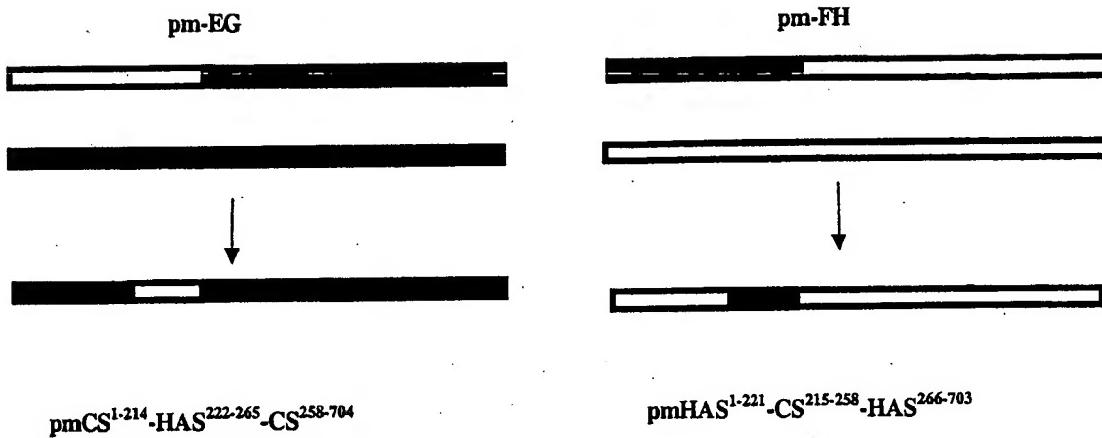


Figure 19

| enzyme | activity | | |
|---------|---------------|----|------------|
| | HAS | CS | GlcUA-Tase |
| pm-BD | - | + | [+] |
| + pm-AC | + | - | [+] |
| + pm-FH | - | + | + |
| pm-EG | - | - | + |
| Pm-JL | + | - | + |
| pm-IK | - | - | + |
| pmCHC | + | + | + |
| pmHCH | not expressed | | |

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SAME
Inventors: Paul L. DeAngelis et al. Group: Unknown
Filed: Herewith Examiner: Unknown
Agent: Douglas J. Sorocco Dkt. No.: 3554.097
SHEET 27 OF 41 Formal Drawings

FIGURE 20



FIGURE 21

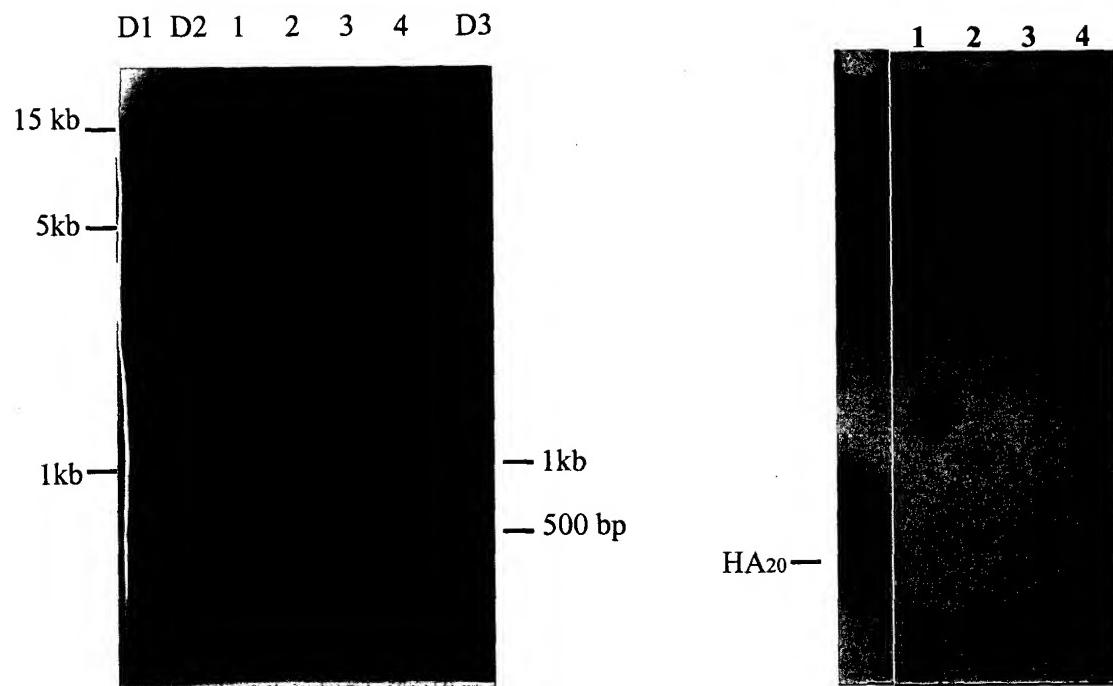


FIGURE 22.
Model of *Pasteurella*
Synthase Polymerization

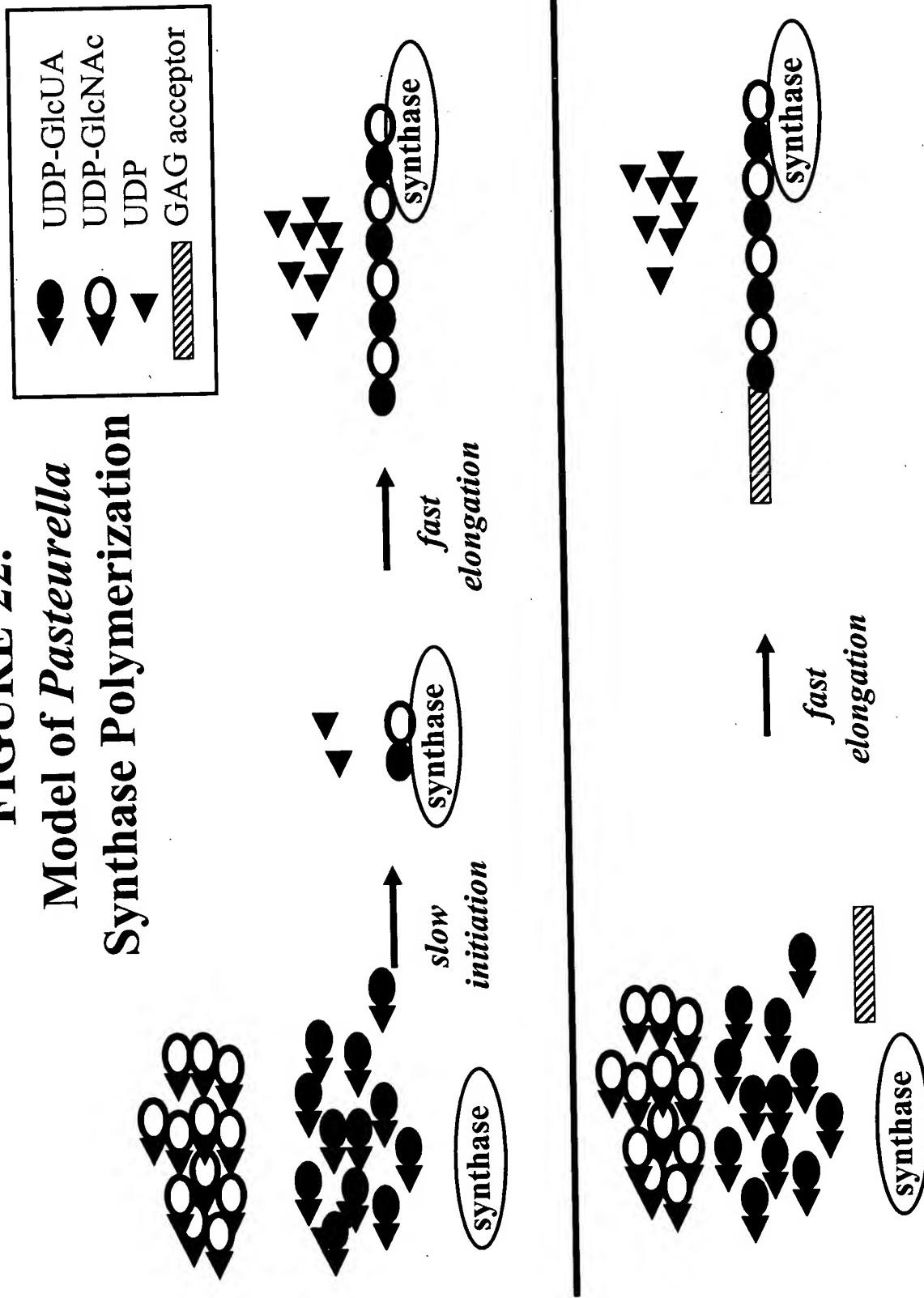


FIGURE 23.

Model of Reaction Synchronization

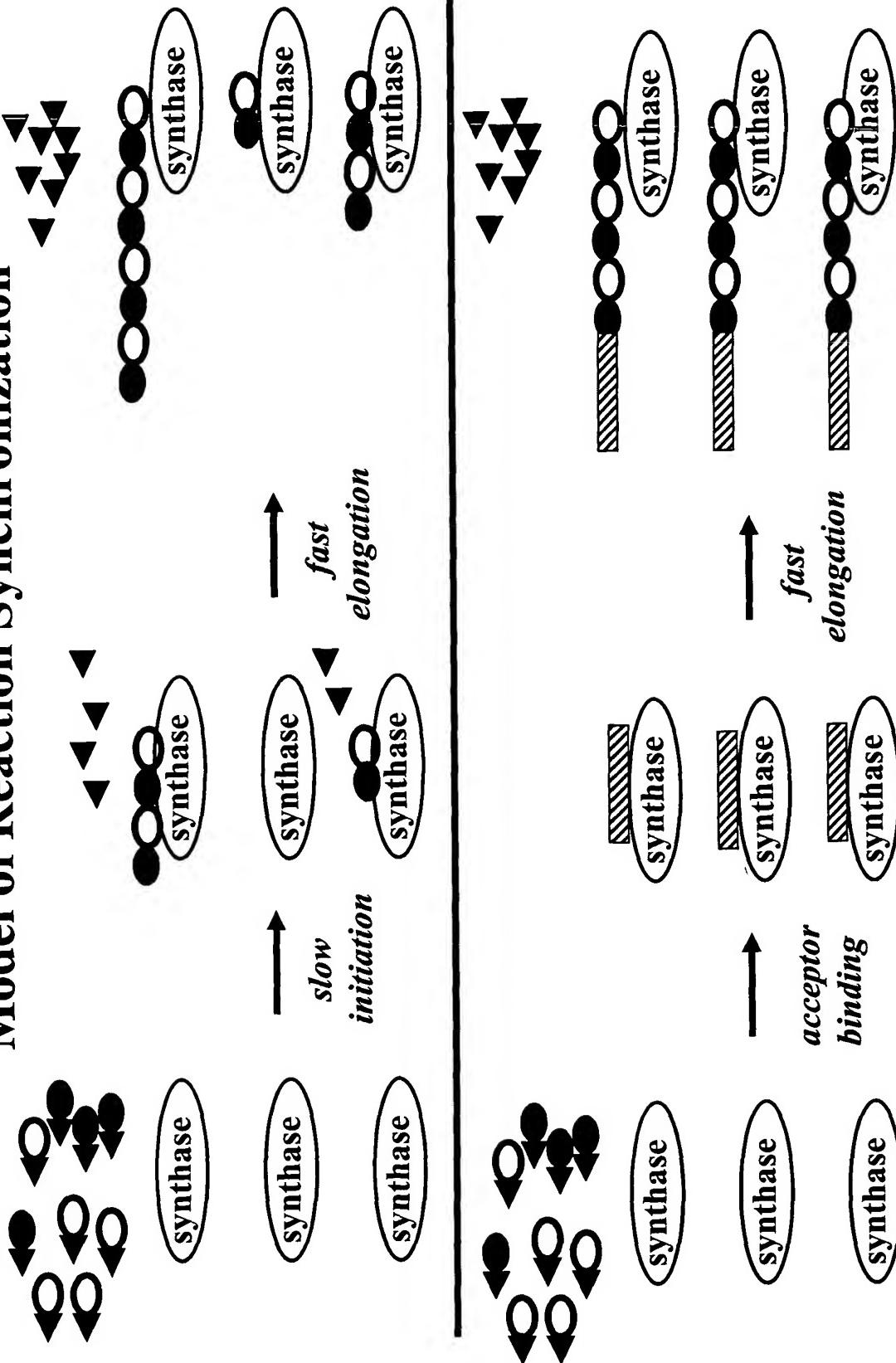


FIGURE 24.
Model of Stoichiometric Control of Polymer Size

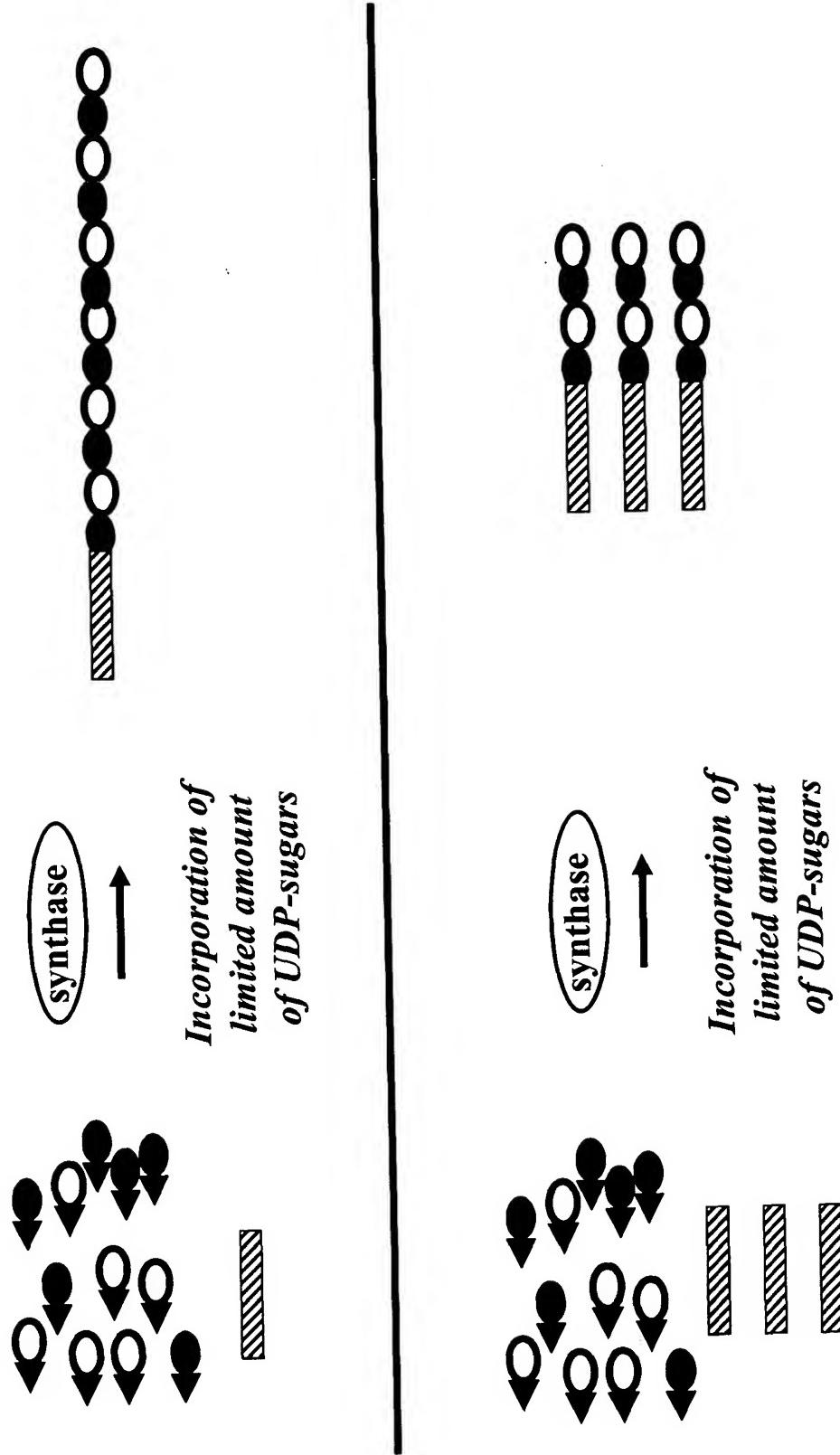


FIGURE 25

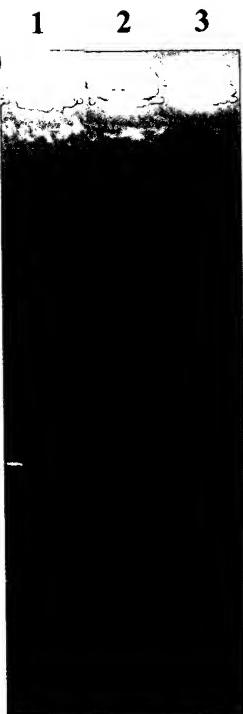
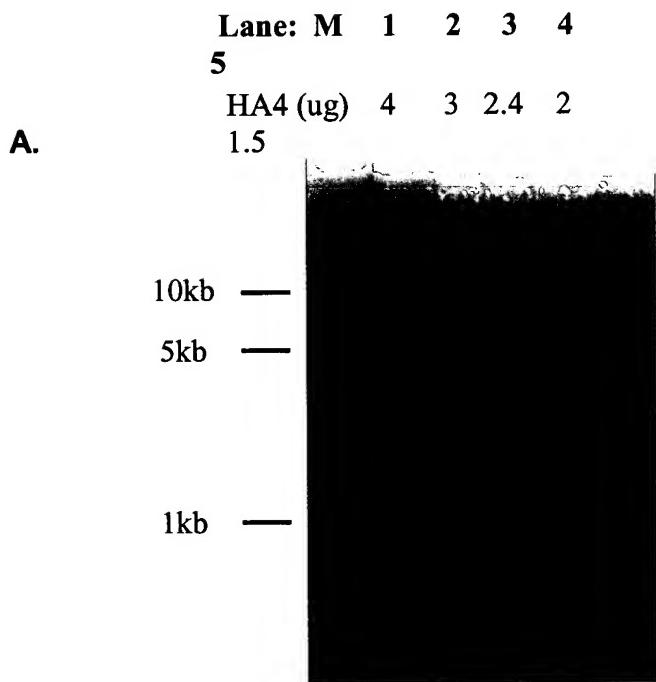


FIGURE 26



B.

| Sample No | Mn | Mw | polydispersity |
|-----------|--------|--------|----------------|
| #1 | 283400 | 283800 | 1.001 |
| #2 | 346400 | 347000 | 1.002 |
| #3 | 422200 | 423700 | 1.004 |
| #4 | 490000 | 493100 | 1.006 |
| #5 | 569700 | 575200 | 1.010 |

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FIGURE 27

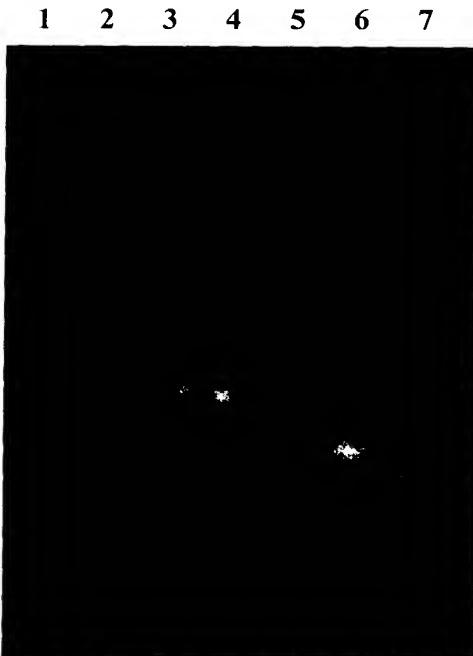


FIGURE 28

572kDa HA (μ g)

5 10 15

970kDa HA (μ g)

5 10 15

Genzyme HA (μ g)

8

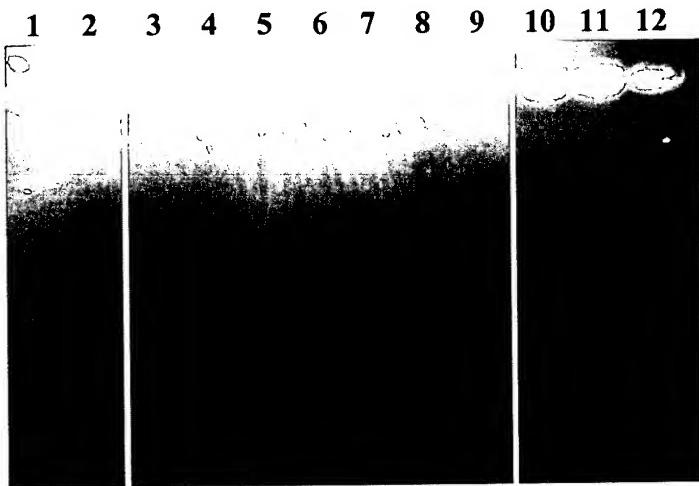


FIGURE 29.
Agarose Gels of Ladders and Migration

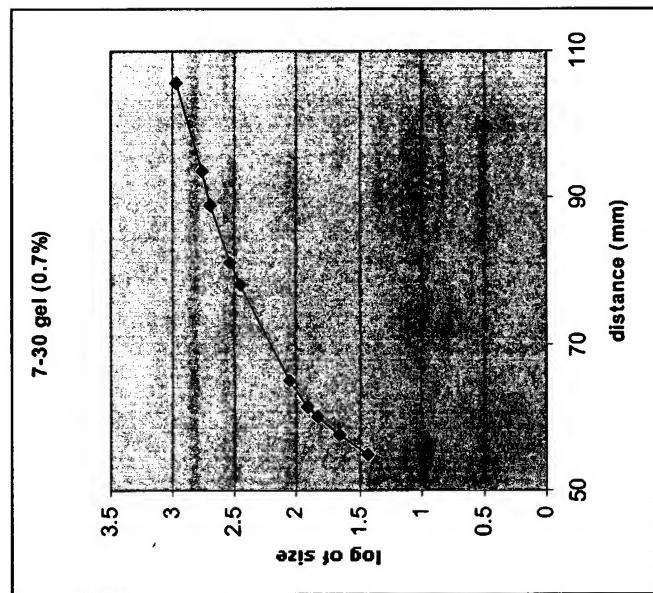
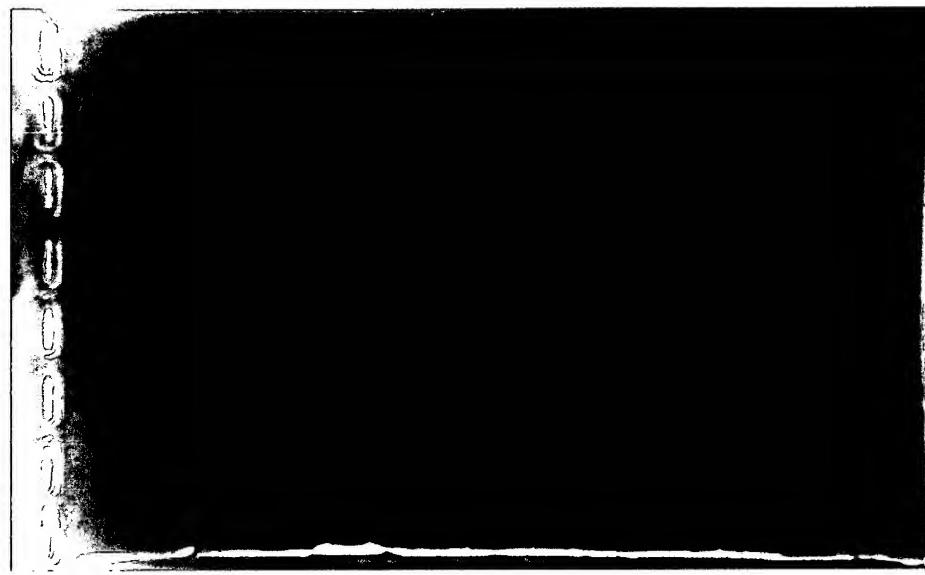
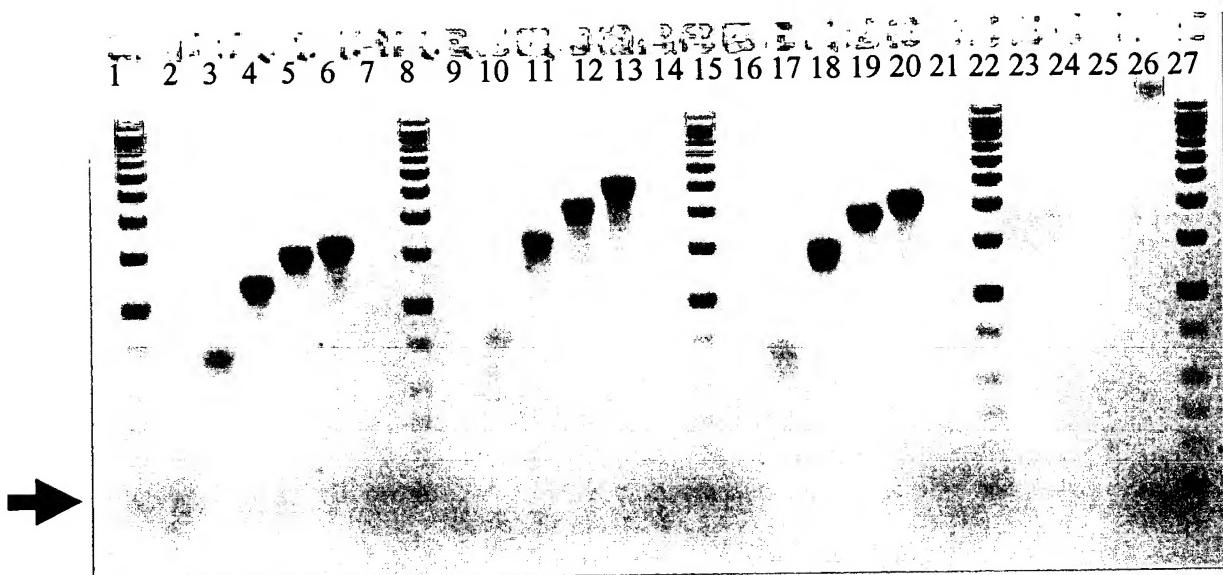


FIGURE 30



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SHEET 38 OF 41 Formal Drawings

FIGURE 31

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26

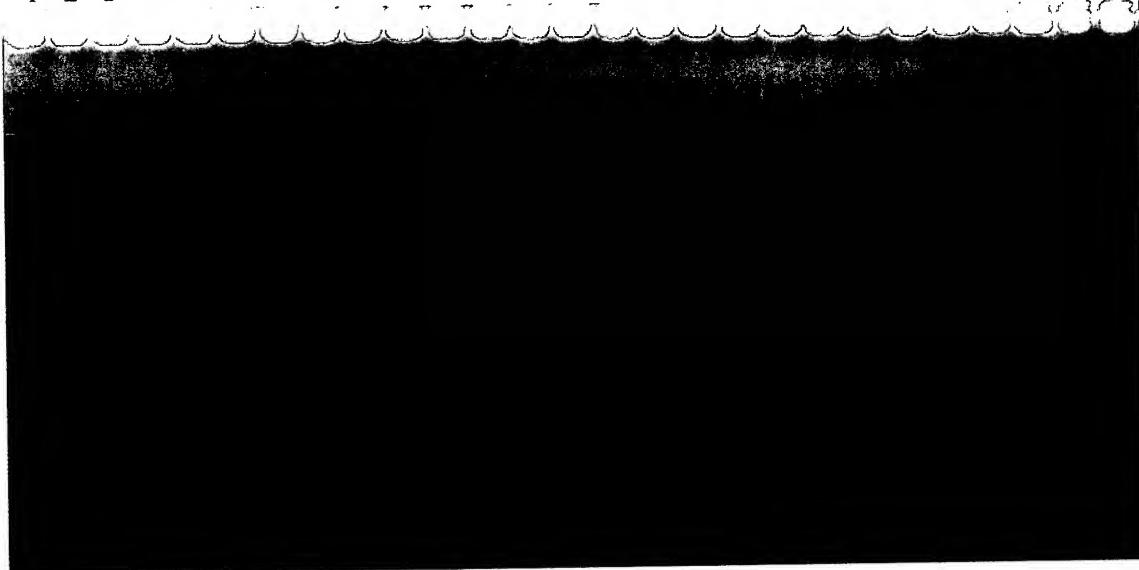
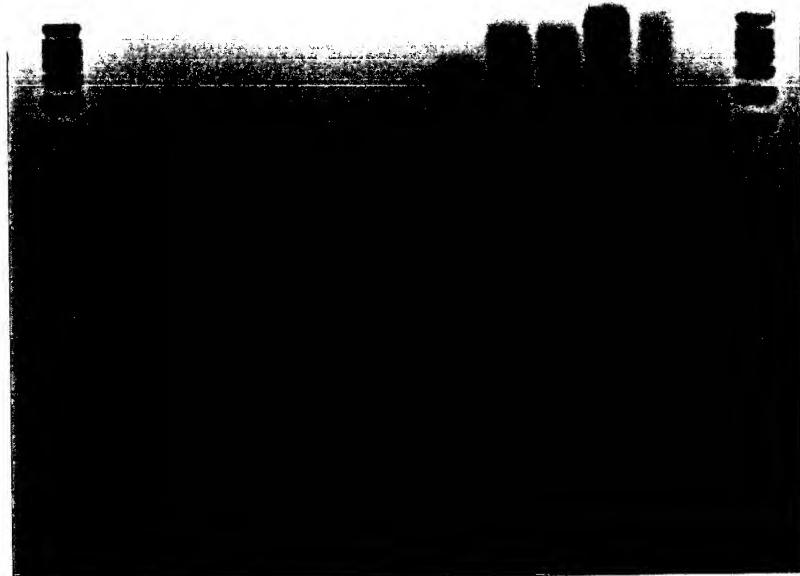


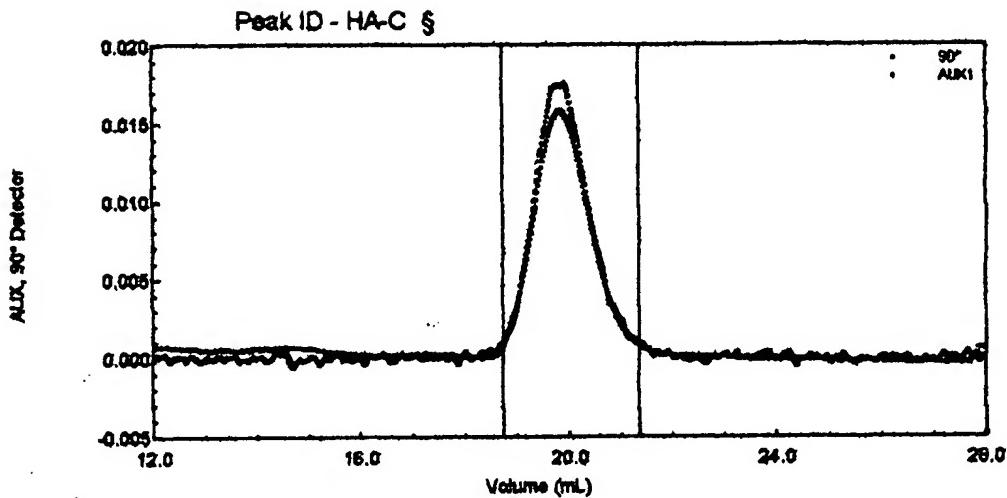
FIGURE 32



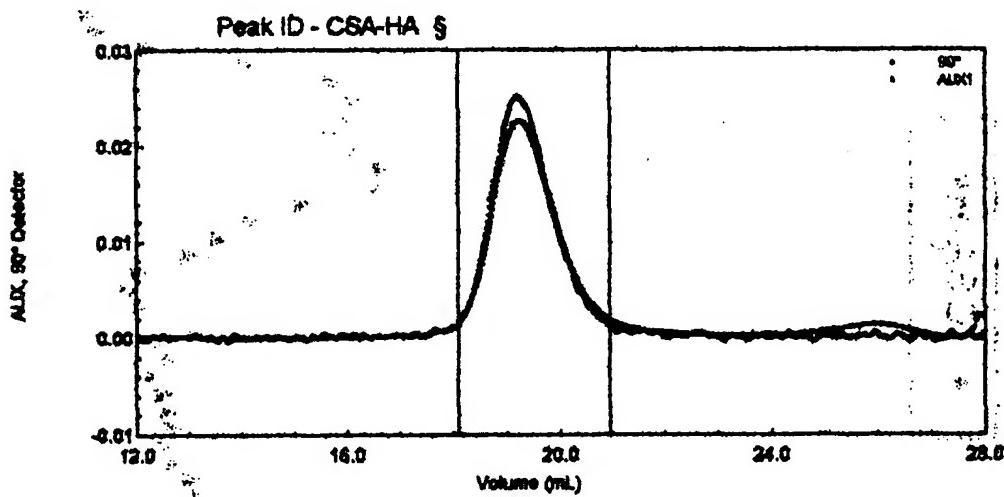
Time: 0 2 4 4 6 O/N 0
Feeding round: - 1 2 1 3 3 -

FIGURE 33

A.



B.



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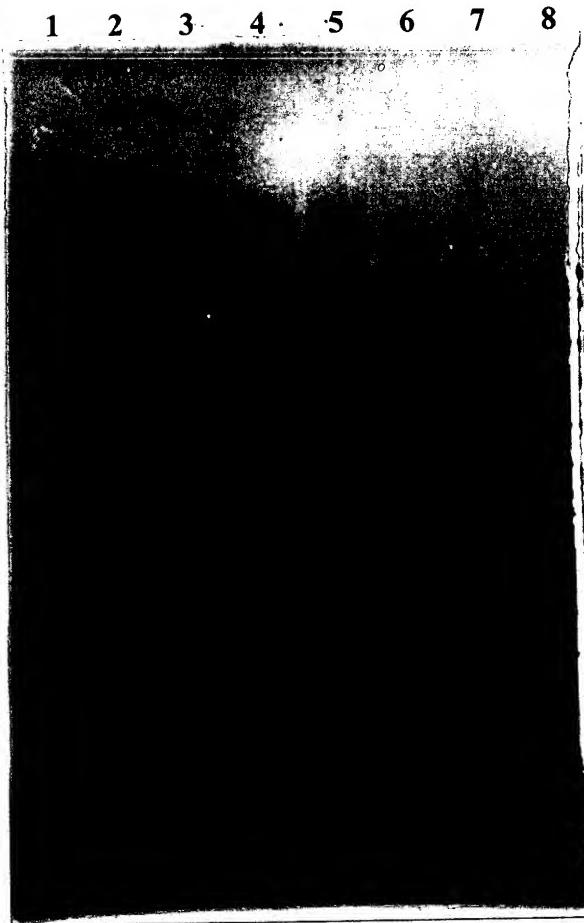


FIG. 34